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<120> Fluorescent protein and color protein

<130> A41347A

<160> 44

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<212> PRT

<213> Montipora sp.

<400> 1

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      35             40             45
Glu Lys Gly Gly Pro Leu Pro Phe Ser Val Asp Ile Leu Ser Ala Ala
      50             55             60
Phe Leu Tyr Gly Asn Arg Cys Met Thr Lys Tyr Pro Gly Gly Ile Val
      65             70             75             80
Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Glu Arg Ser
      85             90             95
Phe Leu Phe Glu Asp Gly Ala Val Cys Thr Ala Ser Ala Asp Ile Arg
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Leu Ser Val Glu Asp Asn Cys Phe Tyr His Glu Ser Lys Phe Ser Gly
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Val Asn Phe Pro Val Asp Gly Pro Val Met Thr Leu Ala Thr Thr Gly

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130	135	140
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Gly Asp Val Thr Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr Arg		
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Cys Gln Phe Asn Ser Asn Tyr Lys Ala Lys Thr Glu Pro Lys Glu Met		
180	185	190
Pro Asp Phe His Phe Val Glu His Lys Ile Val Arg Thr Asp Leu Gly		
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210	215	220
Ser Ala Phe		

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<211> 684

<212> DNA

<213> Montipora sp.

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His Met Glu Gly Cys Val Asn Gly His Glu Phe Thr Ile Lys Gly Glu	
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ggc act ggg caa cct tac gaa ggg aca cag tgt att caa ctc cgt gtg	144
Gly Thr Gly Gln Pro Tyr Glu Gly Thr Gln Cys Ile Gln Leu Arg Val	
35 40 45	

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 Glu Lys Gly Gly Pro Leu Pro Phe Ser Val Asp Ile Leu Ser Ala Ala

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55

60

ttt cta tac gga aac agg tgc atg acc aaa tat cct gga ggc ata gtt 240
 Phe Leu Tyr Gly Asn Arg Cys Met Thr Lys Tyr Pro Gly Gly Ile Val

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70

75

80

gac tat ttc aag aac tca tgc cct gct gga tat aca tgg gaa agg tct 288
 Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Glu Arg Ser

85

90

95

ttt ctc ttt gaa gat ggc gcg gtg tgc aca gca agt gca gat ata cgc 336
 Phe Leu Phe Glu Asp Gly Ala Val Cys Thr Ala Ser Ala Asp Ile Arg

100

105

110

ttg agt gtc gag gat aac tgc ttt tat cac gaa tcc aag ttt agt gga 384
 Leu Ser Val Glu Asp Asn Cys Phe Tyr His Glu Ser Lys Phe Ser Gly

115

120

125

gta aac ttt cct gtt gat gga cct gtg atg aca ctg gcg acg act ggt 432
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130

135

140

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 Trp Glu Pro Ser Ser Glu Lys Met Val Pro Ser Gly Gly Ile Val Lys

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150

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ggg gat gtc acc atg tac ctc ctt ctg aag gat ggt ggg cgt tac cgg 528
 Gly Asp Val Thr Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr Arg

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170

175

tgc cag ttc aac agt aat tac aag gca aag act gag ccg aaa gag atg 576
 Cys Gln Phe Asn Ser Asn Tyr Lys Ala Lys Thr Glu Pro Lys Glu Met

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185

190

cca gac ttt cac ttc gtg gag cat aag atc gta agg acc gac ctc ggt 624
 Pro Asp Phe His Phe Val Glu His Lys Ile Val Arg Thr Asp Leu Gly

195

200

205

ggc cga gac cag aaa tgg caa ctg gtg gga aat tct gct gca tgt gca 672
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220

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Ser Ala Phe

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<211> 232

<212> PRT

<213> Acropora sp.

<400> 3

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Tyr His Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly

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25

30

Val Ala Thr Gly Tyr Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val

35

40

45

Ile Ile Lys Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu

50

55

60

Ser Ser Val Phe His Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala

65

70

75

80

Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr

85

90

95

Glu Arg Ser Phe Leu Phe Glu Asp Gly Ala Val Ala Thr Ala Ser Trp

100	105	110
Asn Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Phe His		
115	120	125
Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile		
130	135	140
Asp Trp Glu Lys Ser Phe Glu Lys Met Thr Val Ser Lys Glu Val Leu		
145	150	155
Arg Gly Asp Val Thr Met Phe Leu Met Leu Glu Gly Gly Gly Ser His		
165	170	175
Arg Cys Gln Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met		
180	185	190
Pro Pro Asn His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly		
195	200	205
Gln Ser Ala Lys Gly Phe Thr Val Lys Leu Glu Ala His Ala Val Ala		
210	215	220
His Val Asn Pro Leu Lys Val Lys		

225

230

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<211> 699

<212> DNA

<213> Acropora sp.

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5

10

15

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Tyr His Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly

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35	40	45	
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Ile Ile Lys Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu			
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Ser Ser Val Phe His Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala			
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Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr			
85	90	95	
gaa agg tca ttt cta ttt gaa gat gga gca gtt gct aca gcc agc tgg 336			
Glu Arg Ser Phe Leu Phe Glu Asp Gly Ala Val Ala Thr Ala Ser Trp			
100	105	110	
aac att cgt ctc gaa gga aat tgc ttc atc cac aat tcc atc ttt cat 384			
Asn Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Phe His			
115	120	125	
ggc gta aac ttt ccc gct gat gga ccc gta atg aaa aag cag aca att 432			
Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile			
130	135	140	
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Asp Trp Glu Lys Ser Phe Glu Lys Met Thr Val Ser Lys Glu Val Leu			
145	150	155	160
aga ggt gat gtg act atg ttt ctt atg ctc gaa gga ggt ggt tct cac 528			
Arg Gly Asp Val Thr Met Phe Leu Met Leu Glu Gly Gly Gly Ser His			

	165	170	175	
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	180	185	190	
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Pro Pro Asn His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly				
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caa agt gca aaa ggc ttt aca gtc aag ctg gaa gca cat gct gtg gct				672
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<213> Acropora sp.				
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Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val				
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Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu				
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Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr						
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Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp						
	100		105		110	
Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His						
	115		120		125	
Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile						
	130		135		140	
Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu						
145		150		155		160
Arg Gly Asp Val Thr Gln Phe Leu Leu Leu Glu Gly Gly Gly Tyr Gln						
	165		170		175	
Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met						
	180		185		190	
Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly						
	195		200		205	
Gln Thr Ala Lys Gly Phe Lys Val Lys Leu Glu Glu His Ala Glu Ala						
	210		215		220	
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<211> 699

<212> DNA

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 Tyr Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly
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 gta gga act gga aac cct tac gaa ggg aaa cag atg tcc gaa tta gtg 144
 Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val
 35 40 45
 atc atc aag tct aag gga aaa ccc ctt cca ttc tcc ttt gac ata ctg 192
 Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu
 50 55 60
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 Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr
 85 90 95
 gaa agg tca ttt cta ttt gag gat gga gga gtt gct aca gcc agc tgg 336
 Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp
 100 105 110
 agc att cgt ctc gaa gga aat tgc ttc atc cac aat tcc atc tat cat 384
 Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His
 115 120 125
 ggc gta aac ttt ccc gct gat gga ccc gta atg aag aag cag aca att 432
 Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile
 130 135 140
 ggc tgg gat aag tcc ttc gaa aaa atg agt gtg gct aaa gag gtg cta 480

Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu
 145 150 155 160
 aga ggt gat gtg act cag ttt ctt ctg ctc gaa gga ggt ggt tac cag 528
 Arg Gly Asp Val Thr Gln Phe Leu Leu Leu Glu Gly Gly Gly Tyr Gln
 165 170 175
 aga tgc egg ttt cac tcc act tac aaa acg gag aag cca gtc gca atg 576
 Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met
 180 185 190
 ccc ccg agt cat gtc gta gaa cat caa att gtg agg acc gac ctt ggc 624
 Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly
 195 200 205
 caa act gca aaa ggc ttc aag gtc aag ctg gaa gaa cat gct gag gct 672
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 210 215 220
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<212> PRT

<213> Acropora sp.

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 Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val

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	50				55					60					
Ser	Thr	Ala	Phe	Gln	Tyr	Gly	Asn	Arg	Cys	Phe	Thr	Lys	Tyr	Pro	Ala
65				70					75					80	
Asp	Met	Pro	Asp	Tyr	Phe	Lys	Gln	Ala	Phe	Pro	Asp	Gly	Met	Ser	Tyr
			85						90					95	
Glu	Arg	Ser	Phe	Leu	Phe	Glu	Asp	Gly	Gly	Val	Ala	Thr	Ala	Ser	Trp
		100						105						110	
Ser	Ile	Arg	Leu	Glu	Gly	Asn	Cys	Phe	Ile	His	Asn	Ser	Ile	Tyr	His
	115						120						125		
Gly	Val	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Lys	Gln	Thr	Ile
	130					135					140				
Gly	Trp	Asp	Lys	Ser	Phe	Glu	Lys	Met	Ser	Val	Ala	Lys	Glu	Val	Leu
145				150					155					160	
Arg	Gly	Asp	Val	Thr	His	Phe	Leu	Leu	Leu	Glu	Gly	Gly	Gly	Tyr	Gln
			165						170					175	
Arg	Cys	Arg	Phe	His	Ser	Thr	Tyr	Lys	Thr	Glu	Lys	Pro	Val	Ala	Met
		180						185						190	
Pro	Pro	Ser	His	Val	Val	Glu	His	Gln	Ile	Val	Arg	Thr	Asp	Leu	Gly
		195						200						205	
Gln	Thr	Ala	Lys	Gly	Phe	Lys	Val	Lys	Leu	Glu	Glu	His	Ala	Glu	Ala
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<212> DNA

<213> Acropora sp.

<400> 8

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Tyr Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly
      20              25              30
gta gga act gga aac cct tac gaa ggg aaa cag atg tcc gaa tta gtg 144
Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val
      35              40              45
atc atc aag tct aag gga aaa ccc ctt cca ttc tcc ttt gac ata ctg 192
Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu
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Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala
      65              70              75              80
gac atg cct gac tat ttc aag caa gca ttc cca gat gga atg tca tat 288
Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr
      85              90              95
gaa agg tca ttt cta ttt gag gat gga gga gtt gct aca gcc agc tgg 336
Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp
      100             105             110
agc att cgt ctc gaa gga aat tgc ttc atc cac aat tcc atc tat cat 384
Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His
      115             120             125
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ggc gta aac ttt ccc gct gat gga ccc gta atg aag aag cag aca att 432
 Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile

130

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140

ggc tgg gat aag tcc ttc gaa aaa atg agt gtg gct aaa gag gtg cta 480
 Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu

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155

160

aga ggt gat gtg act cat ttt ctt ctg ctc gaa gga ggt ggt tac cag 528
 Arg Gly Asp Val Thr His Phe Leu Leu Leu Glu Gly Gly Gly Tyr Gln

165

170

175

aga tgc cgg ttt cac tcc act tac aaa acg gag aag cca gtc gca atg 576
 Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met

180

185

190

ccc ccg agt cat gtc gta gaa cat caa att gtg agg acc gac ctt ggc 624
 Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly

195

200

205

caa act gca aaa ggc ttc aag gtc aag ctg gaa gaa cat gct gag gct 672
 Gln Thr Ala Lys Gly Phe Lys Val Lys Leu Glu Glu His Ala Glu Ala

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cat gtt aac cct ttg aag gtt aaa taa 699

His Val Asn Pro Leu Lys Val Lys

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<210> 9

<211> 232

<212> PRT

<213> *Montipora sp.*

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Val Val Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala			
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Val Phe Asp Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Gln Asp Leu			
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Val Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gln Arg			
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Ser Phe Leu Phe Glu Asp Gly Ala Val Cys Thr Ala Ser Ala Asp Ile			
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Arg Val Ser Val Glu Glu Asn Cys Phe Tyr His Glu Ser Lys Phe His			
115	120	125	
Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr			
130	135	140	
Asn Trp Glu Pro Ser Cys Glu Lys Ile Thr Pro Ile Leu Asn Glu Gly			
145	150	155	160
Ile Leu Lys Gly Asp Val Thr Met Phe Leu Leu Leu Lys Asp Gly Gly			
165	170	175	
Arg Tyr Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ala Asp Ala			
180	185	190	
Lys Lys Met Pro Glu Trp His Phe Ile Gln His Lys Leu Thr Arg Glu			
195	200	205	
Asp Arg Ser Asp Ala Lys His Gln Lys Trp Arg Leu Val Glu Asn Ala			
210	215	220	

Ile Ala Tyr Arg Ser Thr Leu Pro

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230

<210> 10

<211> 699

<212> DNA

<213> *Montipora sp.*

<400> 10

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10

15

cgc atg gaa ggg tgt gtc gat ggg cat aaa ttt gta atc acg ggc gac 96

Arg Met Glu Gly Cys Val Asp Gly His Lys Phe Val Ile Thr Gly Asp

20

25

30

ggc att gga gat cct ttc gaa ggg aaa cag act agt att gat ctg tgt 144

Gly Ile Gly Asp Pro Phe Glu Gly Lys Gln Thr Ser Ile Asp Leu Cys

35

40

45

gtg gtt gaa ggg gga cca ctg cca ttc tcc gaa gat ata ttg tct gct 192

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55

60

gtg ttt gac tac gga aac agg gtc ttt act aaa tat cct caa gac ctt 240

Val Phe Asp Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Gln Asp Leu

65

70

75

80

gtt gac tat ttc aag aac tca tgt cct gct gga tat aca tgg caa agg 288

Val Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gln Arg

85

90

95

tct ttt ctc ttt gaa gat ggt gca gtt tgc aca gcc agt gca gat ata 336

Ser Phe Leu Phe Glu Asp Gly Ala Val Cys Thr Ala Ser Ala Asp Ile

100	105	110	
aga gtg agt gtt gag gag aac tgc ttt tat cac gag tcc aag ttt cat 384			
Arg Val Ser Val Glu Glu Asn Cys Phe Tyr His Glu Ser Lys Phe His			
115	120	125	
gga gtg aac ttt cct gct gat gga cct gtg atg aaa aag atg aca act 432			
Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr			
130	135	140	
aat tgg gaa cca tcc tgc gag aaa atc aca cca ata ctt aat gag ggg 480			
Asn Trp Glu Pro Ser Cys Glu Lys Ile Thr Pro Ile Leu Asn Glu Gly			
145	150	155	160
ata ttg aaa gga gat gtc acc atg ttc ctc ctt ctg aag gat ggt ggg 528			
Ile Leu Lys Gly Asp Val Thr Met Phe Leu Leu Leu Lys Asp Gly Gly			
165	170	175	
cgt tac cgg tgc cag ttc gac aca gtt tac aaa gca aag gct gac gca 576			
Arg Tyr Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ala Asp Ala			
180	185	190	
aaa aag atg ccg gaa tgg cac ttc atc caa cat aag ctc acc cgg gaa 624			
Lys Lys Met Pro Glu Trp His Phe Ile Gln His Lys Leu Thr Arg Glu			
195	200	205	
gac cgc agc gat gct aag cac cag aaa tgg cga ctg gta gaa aat gct 672			
Asp Arg Ser Asp Ala Lys His Gln Lys Trp Arg Leu Val Glu Asn Ala			
210	215	220	
att gca tac cga tcc aca tta ccc tga 699			
Ile Ala Tyr Arg Ser Thr Leu Pro			
225	230		
<210> 11			
<211> 232			

<212> PRT

<213> Actinia equina

<400> 11

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			20					25					30		
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		35					40					45			
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	50					55					60				
Gly	Ser	Lys	Thr	Phe	Ile	Lys	His	Val	Ser	Gly	Ile	Pro	Asp	Tyr	Phe
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Lys	Asp	Ser	Leu	Pro	Glu	Gly	Tyr	Thr	Trp	Glu	Arg	Thr	Gln	Ile	Tyr
			85						90				95		
Glu	Asp	Gly	Gly	Tyr	Leu	Thr	Ile	His	Gln	Asp	Thr	Ser	Ile	Gln	Gly
		100						105					110		
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		115					120						125		
Asn	Gly	Pro	Val	Met	Gln	Lys	Lys	Thr	Ala	Gly	Trp	Glu	Pro	Cys	Val
	130					135					140				
Glu	Met	Leu	Tyr	Pro	Arg	Asp	Gly	Val	Leu	Cys	Gly	Gln	Ser	Leu	Met
145				150						155				160	
Ala	Leu	Lys	Cys	Thr	Asp	Gly	Asn	His	Leu	Thr	Ser	His	Leu	Arg	Thr
			165						170				175		
Thr	Tyr	Arg	Ser	Arg	Lys	Pro	Ala	Asn	Ala	Val	Asn	Met	Pro	Lys	Phe
		180							185				190		

His Phe Gly Asp His Arg Ile Glu Ile Leu Lys Glu Ala Glu Pro Gly

195

200

205

Lys Phe Tyr Glu Gln Tyr Glu Ser Ala Val Ala Arg Tyr Cys Glu Ala

210

215

220

Ala Pro Ser Lys Leu Gly His His

225

230

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<212> DNA

<213> Actinia equina

<400> 12

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Met Ser Ser Leu Val Lys Lys Asp Met Cys Ile Lys Met Thr Met Glu

1

5

10

15

ggg aca gta aat ggt cac cac ttc aag tgt gta gga gaa gga gaa ggc 96

Gly Thr Val Asn Gly His His Phe Lys Cys Val Gly Glu Gly Glu Gly

20

25

30

aag cca ttt gaa ggt acc cag gag gaa aag ata aga atc act gaa gga 144

Lys Pro Phe Glu Gly Thr Gln Glu Glu Lys Ile Arg Ile Thr Glu Gly

35

40

45

ggt ccc tta cca ttt gcg tac gat att ttg gca cct tgt tgc atg tat 192

Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Ala Pro Cys Cys Met Tyr

50

55

60

gga agc aaa acc ttc atc aag cat gtc tca ggg att cca gat tac ttc 240

Gly Ser Lys Thr Phe Ile Lys His Val Ser Gly Ile Pro Asp Tyr Phe

65

70

75

80

aag gat tct tta cct gaa gga tac act tgg gaa aga acc caa atc tac 288

Ala Pro Ser Lys Leu Gly His His

225

230

<210> 13

<211> 224

<212> PRT

<213> *Lobophytum crassum*

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Met Ser Val Ile Lys Gln Glu Met Lys Ile Lys Leu His Met Glu Gly

1

5

10

15

Asn Val Asn Gly His Ala Phe Val Ile Glu Gly Asp Gly Lys Gly Lys

20

25

30

Pro Tyr Asp Gly Thr Gln Thr Leu Asn Leu Thr Val Lys Glu Gly Ala

35

40

45

Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Asn Ala Phe Gln Tyr Gly

50

55

60

Asn Arg Ala Phe Thr Lys Tyr Pro Ala Asp Ile Pro Asp Tyr Phe Lys

65

70

75

80

Gln Thr Phe Pro Glu Gly Tyr Ser Trp Glu Arg Thr Met Ser Tyr Glu

85

90

95

Asp Asn Ala Ile Cys Asn Val Arg Ser Glu Ile Ser Met Glu Gly Asp

100

105

110

Cys Phe Ile Tyr Lys Ile Arg Phe Asp Gly Lys Asn Phe Pro Pro Asn

115

120

125

Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu

130

135

140

Met Met Tyr Val Arg Asp Gly Phe Leu Met Gly Asp Val Asn Met Ala

145

150

155

160

Leu Leu Leu Glu Gly Gly Gly His His Arg Cys Asp Phe Lys Thr Ser
165 170 175

Tyr Lys Ala Lys Lys Val Val Gln Leu Pro Asp Tyr His Tyr Val Asp
180 185 190

His Arg Ile Glu Ile Leu Ser His Asp Arg Asp Tyr Ser Lys Val Lys
195 200 205

Leu Tyr Glu Asn Ala Val Ala Arg Tyr Ser Leu Leu Pro Ser Gln Ala
210 215 220

<210> 14

<211> 675

<212> DNA

<213> *Lobophytum crassum*

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Met Ser Val Ile Lys Gln Glu Met Lys Ile Lys Leu His Met Glu Gly

1 5 10 15

aat gta aac ggt cat gca ttt gtg att gaa gga gat gga aaa gga aag 96

Asn Val Asn Gly His Ala Phe Val Ile Glu Gly Asp Gly Lys Gly Lys

20 25 30

cct tac gat ggg aca cag act tta aac ctg aca gtg aaa gaa ggc gca 144

Pro Tyr Asp Gly Thr Gln Thr Leu Asn Leu Thr Val Lys Glu Gly Ala

35 40 45

cct ctc cct ttt tct tac gac atc ttg aca aat gcg ttc cag tac gga 192

Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Asn Ala Phe Gln Tyr Gly

50 55 60

aat aga gca ttc act aaa tat cca gcc gat ata cca gac tat ttc aag 240

Asn Arg Ala Phe Thr Lys Tyr Pro Ala Asp Ile Pro Asp Tyr Phe Lys

65	70	75	80
cag acg ttt ccc gag ggg tat tca tgg gaa aga acc atg agt tat gaa	288		
Gln Thr Phe Pro Glu Gly Tyr Ser Trp Glu Arg Thr Met Ser Tyr Glu			
85	90	95	
gac aac gcc att tgc aac gtg aga agc gag atc agc atg gaa ggc gac	336		
Asp Asn Ala Ile Cys Asn Val Arg Ser Glu Ile Ser Met Glu Gly Asp			
100	105	110	
tgc ttt atc tat aaa att cgg ttt gat ggc aag aac ttt ccc ccc aat	384		
Cys Phe Ile Tyr Lys Ile Arg Phe Asp Gly Lys Asn Phe Pro Pro Asn			
115	120	125	
ggt cca gtt atg cag aag aaa act ttg aag tgg gaa cca tcc act gag	432		
Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu			
130	135	140	
atg atg tac gtg cgt gat ggg ttt ctg atg ggt gat gtt aac atg gct	480		
Met Met Tyr Val Arg Asp Gly Phe Leu Met Gly Asp Val Asn Met Ala			
145	150	155	160
ctg ttg ctt gaa gga ggt ggc cat cac cga tgt gac ttc aaa act tcc	528		
Leu Leu Leu Glu Gly Gly Gly His His Arg Cys Asp Phe Lys Thr Ser			
165	170	175	
tac aaa gcg aaa aag gtt gtg cag ttg cca gat tat cac tat gtg gac	576		
Tyr Lys Ala Lys Lys Val Val Gln Leu Pro Asp Tyr His Tyr Val Asp			
180	185	190	
cat cgt atc gag atc ttg agc cat gac agg gat tac agc aaa gtc aag	624		
His Arg Ile Glu Ile Leu Ser His Asp Arg Asp Tyr Ser Lys Val Lys			
195	200	205	
ctg tat gag aat gcg gtt gct cgc tat tct ttg ctg cca agt cag gcc	672		
Leu Tyr Glu Asn Ala Val Ala Arg Tyr Ser Leu Leu Pro Ser Gln Ala			

210	215	220	
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gaaggrtgyg tcaayggrca y		21	
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acvggdcat ydgvaagaaa rtt		23	
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ggccacgcgt cgactagtac gggiigggii gggiig		36	
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ccatcttcaa agagaaaaga ccttt 25

<210> 19

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<400> 19

ggccacgcgt cgactagtac 20

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catgagttct tgaaatagtc aac 23

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atggctcttt caaagcgagg tg 22

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gggggatccg accatggctc tttcaaagcg aggtg 35

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tagaaatgac ctttcatatg acattc 26

<210> 24

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tctgtttcca tattgaaagg ctg	23
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atgggtgtctt attcaaagca aggcacgca ca	32
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atggctcttt caaagcacgg tc 22

<210> 32

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<210> 33

<211> 23

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<400> 33

ggiwsbgtia ayggvcayda ntt 23

<210> 34

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gtcittcttyt gcaciacigg iccatydgva ggaaa 35

<210> 35

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ccttgaaaat aaagctatct 20

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ccctgtatgc ttgtgtcctg 20

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cccggatccg accatggtgt cttcattggt taagaa 36

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<400> 38

grraggiwsb gthaayggvc a

21

<210> 39

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<400> 39

aactggaaga attcgcggcc gcaggaa

27

<210> 40

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<223> Description of Artificial Sequence: Synthetic DNA

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gtcittcttyt gcaciacigg iccatydgva ggaaa

35

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cttctcacgt tgcaaattgc 20

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<400> 44

cccggatccg atgagtgtga ttacawcaga aatgaagatg gagg 44